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RAW SEQUENCE LISTING DATE: 06/06/2000
PATENT APPLICATION: US/09/579,383 TIME: 17:03:39

Input Set : A:\02600101.app
Output Set: N:\CRF3\06062000\1579383.raw

3 <110> APPLICANT: Vinetz, Joseph M
5 <120> TITLE OF INVENTION: Plasmodium Sp. Chitinase
7 <130> FILE REFERENCE: 026.00101
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/579,383
C--> 10 <141> CURRENT FILING DATE: 2000-05-26
12 <150> PRIOR APPLICATION NUMBER: US 60/136,508
13 <151> PRIOR FILING DATE: 1999-05-28
15 <150> PRIOR APPLICATION NUMBER: US 60/180,051
16 <151> PRIOR FILING DATE: 2000-02-03
18 <160> NUMBER OF SEQ ID NOS: 26
20 <170> SOFTWARE: PatentIn Ver. 2.1
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23 <211> LENGTH: 1137
24 <212> TYPE: DNA
25 <213> ORGANISM: Plasmodium falciparum
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30 cgtaaatta tcaaaaacgtt taaagaaatcc ggtaaaggta tcataccaggg ttactatccg 180
31 tcctgggtga gctataatca caacctgaag gacctaacc cgaacctgaa cgtggttcac 240
32 atgagcttg ctaaaatgga tttaaagtac gactccattg aatccatcgta aggttagcccg 300
33 ctgcgttta aaaggctgtat tgccgttggg tatattgttgc tgaatgatgc cttcaatgtat 360
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43 gcatactatg gtaaaaaaggta cgattacgtt atcatcatgg gcttcacccgtatgttcccg 960
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45 actgaaaaca aactgaataa acgcgcgatg ggittcggcc tgggtctct gtccagcgac 1080
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52 <213> ORGANISM: Plasmodium gallinaceum
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61 gcaaaaacata tggatgttccaaacccatgttgcataatccat tataatatttc attttgtccgc 420

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124          165          170          175
126 Gly Ser Phe Asp Gly Leu Asn Asp Lys Glu Lys Ala Asp Phe Phe Val
127          180          185          190
129 Gln Tyr Val Thr Lys Leu Arg Glu Tyr Met Cys Asp Asp Lys Leu Ile
130          195          200          205
132 Ser Ile Ser Gln Ser Ser Asn Gly Ala Leu Ser Cys Ile Gly Phe Asn
133          210          215          220
135 Asp Pro Lys Lys Ile Cys Met Asp Asp Glu Ala Pro Tyr Asn Ser Lys
136 225          230          235          240
138 Tyr Phe Asn Lys Pro Asp Val Lys Lys Glu Leu Leu Arg Ala Ala Gln
139          245          250          255
141 Met Ala Ser Ala Gly Gly Ala Ile Tyr Leu Met Asn Asn Leu Lys Asp
142          260          265          270
144 Met Ile Asp Met Val Phe Val Gln Thr Phe Asn Tyr Thr Asn Ser Thr
145          275          280          285
147 Asp Ser Thr Val Met Lys Glu Leu Tyr Asp Ser Tyr Ala Tyr Tyr Gly
148          290          295          300
150 Lys Lys Tyr Asp Tyr Val Ile Ile Met Gly Phe Thr Leu Met Phe Pro
151 305          310          315          320
153 Ser Thr Pro Phe Asn Pro Asn Asp Lys Met Leu Val Lys Ser Ile Gly
154          325          330          335
156 Asp Phe Val Lys Thr Glu Asn Lys Leu Asn Lys Arg Ala Asp Gly Phe
157          340          345          350
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176          20          25          30
178 Leu Gly Ile Ile Arg Glu Asn Lys Asn Lys Thr His Gln Thr Glu Ile
179          35          40          45
181 His Glu Ser Phe Ser His Leu Lys Ser Asn Asn Ser Asn Phe Val Glu
182          50          55          60
184 Tyr Gly Ser Tyr Cys Gly Asp Gly Cys Asn Ser Arg Ile Thr Lys Asn
185 65          70          75          80
187 Asn Lys Asn Ile Asn Lys Asn Asp Arg Lys Ser Pro Arg Gln Ile Leu
188          85          90          95
190 Glu Glu Tyr Lys Lys Arg Lys Gln Gly Ile Ile Ala Gly Tyr Tyr Gly
191          100         105         110
193 Ser Trp Asn Ser Gln Gly Asp Arg Ala Lys His Met Ile Asp Ser Asn
194          115         120         125
196 Pro Met Val Ser Ile Leu Tyr Ile Ala Phe Ala Arg Ile Asn Met Leu

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| 199 | Tyr Asp Val Ser Arg Pro Phe Asn Gly Arg Gln Arg Phe Leu Leu Arg | | |
| 200 | 145 | 150 | 155 |
| 202 | Lys His Gly Leu Glu Tyr Glu Thr Tyr Gly Met Met Leu Asn Glu Ile | | 160 |
| 203 | 165 | 170 | 175 |
| 205 | Arg Arg Ile Arg Lys Val Arg Pro Asp Val Ile Ile Leu Leu Ser Leu | | |
| 206 | 180 | 185 | 190 |
| 208 | Gly Gly Glu Thr Tyr Met Ile Asp Ile Glu Lys Glu Ile Asp Tyr Val | | |
| 209 | 195 | 200 | 205 |
| 211 | Asp Lys Ile Leu Lys Leu Val Asn Asp Phe Asp Leu Asp Gly Val Asp | | |
| 212 | 210 | 215 | 220 |
| 214 | Ile Asp Trp Glu Pro His Gly Lys Phe Tyr Asn Leu Asn Glu Leu Asn | | |
| 215 | 225 | 230 | 235 |
| 217 | Phe Ser Asn Tyr Tyr Ile Lys Leu Ile Asn Leu Leu Arg Lys Thr Ile | | 240 |
| 218 | 245 | 250 | 255 |
| 220 | Pro Glu Glu Lys Leu Ile Ser Ile Ser Gly Ser Ser Asn Ala Ala Leu | | |
| 221 | 260 | 265 | 270 |
| 223 | Ser Cys Val Ser Gly Val Ala Ser Phe Cys Lys Asp Glu Glu Ser Pro | | |
| 224 | 275 | 280 | 285 |
| 226 | Tyr Asn Thr Lys Phe Leu Ser Glu Gln Ile Glu Thr Asn Lys Glu Leu | | |
| 227 | 290 | 295 | 300 |
| 229 | His Arg Ala Ala Ala Met Leu Ser Ala Gly Thr Phe Ile Asn Ile Phe | | |
| 230 | 305 | 310 | 315 |
| 232 | Asn Thr Ala Lys Glu Lys Ile Asp Leu Val Phe Ile Gln Thr Tyr Asn | | 320 |
| 233 | 325 | 330 | 335 |
| 235 | Leu Glu Thr Thr Asn Pro Asp Ile Met Val Asp Met Tyr Leu Ser His | | |
| 236 | 340 | 345 | 350 |
| 238 | Leu Tyr Phe Gly Leu Lys Tyr Asn Ile Thr Ile Ile Leu Gly Phe Ser | | |
| 239 | 355 | 360 | 365 |
| 241 | Leu Glu His Asn Arg Gly Gly Phe Ser Pro Glu Asn Lys Glu Leu Leu | | |
| 242 | 370 | 375 | 380 |
| 244 | Glu Leu Val Gly Lys Thr Ile His Asp Lys Asn Gln Asn Asn Asn Arg | | |
| 245 | 385 | 390 | 395 |
| 247 | Ala Asp Gly Ile Gly Ile Trp His Leu Phe Met Lys Glu Gln Leu Pro | | 400 |
| 248 | 405 | 410 | 415 |
| 250 | Thr Gly Ser Phe Asp Val Asp Ile Phe Leu Thr Asn Ile Trp Lys His | | |
| 251 | 420 | 425 | 430 |
| 253 | Leu Asn Pro Glu Val Gln Thr Pro Lys Asp Leu Thr Ile Thr Glu Asn | | |
| 254 | 435 | 440 | 445 |
| 256 | Pro Glu Asp Cys Ser Thr Ile Asp Glu Tyr Val Pro Gly Leu Val Ile | | |
| 257 | 450 | 455 | 460 |
| 259 | Pro Thr Ile Gly Ile Tyr Tyr Lys His Asn Asp Ala Ile Trp Lys Thr | | |
| 260 | 465 | 470 | 475 |
| 262 | Arg Ser Tyr Ser Ile His Ala Pro Gly Val Asp Arg Tyr Glu Trp Asp | | 480 |
| 263 | 485 | 490 | 495 |
| 265 | Leu Val Lys Val Cys Tyr Glu Lys Ile Cys Asp Gly Lys Ala Ala His | | |
| 266 | 500 | 505 | 510 |
| 268 | Tyr Tyr Asn Thr Asp Tyr Lys Glu Ser Ser Ile Ile Trp Lys Gly | | |
| 269 | 515 | 520 | 525 |

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271 Glu Pro Tyr Leu Ile Lys Trp Trp Gln Gln Gly Pro Pro Glu Gly Gln
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292 ttTTTGTtT ttTGTCTTtT ttGTTCTTtT cTTTTCTTtT tagCTTCat 180
293 aATTCTTTC caATTTTTtT gTTAATTTg TTGTCCTTg TATGTTATCT TAATATTAC 240
294 attTCATTA tagTAGATA taATTTTa gAAAATGAA tTTTAAATA tCAATATTtT 300
295 TAATTATAGT ATCCATCTTg TATTCGCAA ATCCAGAAC CTGAAAGGA AAAAATAATA 360
296 TAAATAATC ATTGGAAATA ATACGGAAAT AAAAATAATA aACTCATCAA ACGGAAATAC 420
297 atGAGTCTTtT tcACATTTT aATCgAATA atAGATAATTtT tgAGATAATtT ggATCTTtT 480
298 gCGGAGATGG GTGTAACtTtT AGAATACAA AAAATAATAA AAATAATAAT AAAATAATA 540
299 gAAAATCACC AAGACAAATT ttagAGGAGT ATAAAAAAAG gAAACAAGGT ATTATAGCAG 600
300 gATACATGG TTCATGGAAc AGTCAGGTG ATAGAGCAA ACATATGATT gATCaaACC 660
301 CAATGGTGC AATTtTATAT ATTGCAATTG CTGCAATTAA TATGTTATAT GATGATCTA 720
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303 atGGTATGAT GCTTAATGAA ATTAGACGTA TCAgAAAAGT ACgTCCAGAT gTAATTATC 840
304 ttttATCCTT AGGTGGAGAA ACCATATGTA TAGATATGAA AAAAGAAATT GATTATGTGG 900
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307 TTAACTTGTtT AGAAAATACT ATCCGGAAG AAAAGTTAT tTCATTTCTT gGTTCATCAA 1080
308 ATGCTGCATT ATCATGCgtT TCAGGAGTTG CATCTTCTG TAAAGATGAA GAATCTCCAT 1140
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310 CGATGTTAC AGCAGGAAT TTtTAATAA tTTTAAATAC AGCaaAGGAG AAAATAGATC 1260
311 TTGTTATTAAT TCAACATAC AATTAGAAA CTCAAAATCC AGATATAATG GTAGATATGT 1320
312 ACTTATCCCA TTTATTTT GGTtAAAT ATAACATCAC AACATATTA GGTTTTCT 1380
313 TAGAACATAA CAGAGGTGGA TTTAGTCCCG AAAATAAGA ATTATTAGAA TTGGTAGGAA 1440
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321 AACCATAATTtT ATTAAATGG TGGCAACAAg GACCTCCGGA AGGTcAGGCA CTAGAGTCAT 1920
322 ACACAAACtT AGATGATCC AATGTCAG GGTAGAAAGA ATGGAATAAA AAATATCCAC 1980
323 ATAAACCACT AGAAGTAGAG GAAcAAATAG AACAAGAAGT GGATTtACCA TTACAATAAA 2040
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325 AAATATAACAA AAATAATAAA GTAAAATAAA CATATTACCA TGGTAAAATAA AGATAAATTA 2160

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:621 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
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